REMARKS

1. Status of claims

After entry of the above amendment, claims 12-14 are pending.

2. Support for amendment

The amendment to the specification is supported by the current status of United States patent application 09/630,983

3. Objection to the specification

The Examiner objected to the specification for not reporting the number of the patent issued from United States patent application 09/630,983. By the above amendment to the specification, this information has been reported and Applicants submit the basis for this objection has been removed.

4. Objection to the claims

The Examiner objected to claims 12-14 for being accompanied by inappropriate status identifiers. As shown in the listing of the claims, the status identifiers for claims 12-14 have been updated to read "(Previously presented)" and Applicants submit the basis for this objection has been removed.

5. *Claim rejections under 35 U.S.C. § 112*

The Examiner rejected claims 12-14 under 35 U.S.C. § 112, first paragraph, as failing to comply with the written description requirement, for reasons of record set forth in the Office Action mailed December 6, 2005. Applicants traverse this rejection.

The Examiner alleged that "sequences of at least about 90% similarity or identity to [SEQ ID NO:11 or encoded by a coding region having a structure having at least about 90% identity with SEQ ID NO:12] which can be transformed into a host yeast such that the yeast is capable of producing ascorbic acid when grown in a medium comprising an ascorbic acid precursor" are not clear to one of ordinary skill in the art (Detailed Action, p. 8).

Applicants disagree. The claims recite, among other features, proteins having both the functional characteristics of an LGDH (NAD^+-dependent enzymes capable of catalyzing the conversion of L-galactose to L-galactono-1,4-lactone) *and* a structure having at least about 90% similarity or at least about 90% identity to SEQ ID NO:11 or being encoded by a coding region having a structure having at least about 90% identity with SEQ ID NO:12. Both the functional characteristic and the structural characteristic are clear to the skilled artisan and are described in the specification in a way that reasonably conveys to the skilled artisan that Applicants had possession of the claimed invention at the time of filing. Though not every specific protein meeting both the functional characteristic and the structural characteristic is recited, attempting to recite every specific protein would be both unduly prolix and unnecessary. The skilled artisan can routinely determine whether a particular protein having the recited structural characteristic also has the recited functional characteristic, or vice versa. The observation that no sequence motifs characterizing LGDHs were known as of the filing date of the present application is irrelevant. The skilled artisan would understand that Applicants possessed *both* a method of

using an LGDH having SEQ ID NO:11 or being encoded by a coding region having SEQ ID NO:12 *and* using an LGDH having or being encoded by a sequence having some variation relative to SEQ ID NO:11 or SEQ ID NO:12, respectively. Use of the latter LGDHs would be conveyed to the ordinary skilled artisan in light of the general knowledge in the art that minor variations in a peptide or nucleic acid sequence (such as about 10%) may have little or no negative impact on the function of an enzyme. Any deleterious variations of SEQ ID NO:11 or SEQ ID NO:12, i.e., such that the enzyme having or being encoded by such hypothetical variations does not enable a yeast expressing the enzyme to produce ascorbic acid when grown in a medium containing an ascorbic acid precursor, would eliminate LGDH function from the enzyme and thus exclude it from the specification's teachings of use of an enzyme having an LGDH function.

For at least these reasons, Applicants request this rejection of claims 12-14 be withdrawn.

6. Claim rejections under obviousness-type double patenting

The Examiner provisionally rejected claims 12-14 on the ground of non-statutory obviousness-type double patenting over claims 7 and 11-14 of copending US 10/606,302. The Examiner also rejected claims 12-14 on the ground of non-statutory obviousness-type double patenting over claims 1-9 of US 6,630,330.

Applicants herewith submit a terminal disclaimer over US 10/606,302 and US 6,630,330 and Applicants submit the basis for this objection has been removed.

7. Claim rejections under 35 U.S.C. § 102

The Examiner rejected claims 12-14 under 35 U.S.C. § 102(b) as being anticipated by Smirnoff *et al.*, WO 99/33995 ("Smirnoff"). Applicants traverse this rejection.

Smirnoff teaches an isolated L-galactose dehydrogenase (p. 3, second full paragraph) comprising at least a portion of an N-terminal 19-mer polypeptide extracted from pea (*Pisum sativum*) (p. 6, fifth paragraph; p. 10, example 3; p. 24, SEQ. 1), and a yeast expressing the polypeptide (p. 4, fourth paragraph). Smirnoff also teaches the *Agrobacterium*-mediated transformation of *plants* by use of vectors pPB1121 or pGPTV-kan, into which a coding sequence for an L-galactose dehydrogenase *may* be inserted (p. 21, second full paragraph).

To anticipate the present claims, Smirnoff must teach every element thereof. Smirnoff does not. Smirnoff teaches the use of an LGDH having an N-terminal 19-mer (SEQ. 1) having 72% identity with amino acids 5-22 of an *Arabidopsis thaliana* putative peptide of unknown function, Genbank Accession No. 3549669. Therefore, Smirnoff's SEQ. 1 does not have at least 90% identity with amino acids 5-22 of the *Arabidopsis* putative peptide. Further, it cannot be determined whether Smirnoff's SEQ. 1 has at least 90% identity with the entire *Arabidopsis* putative peptide. In addition, Smirnoff's statement that "it is likely that this *Arabidopsis thaliana* putative protein is, in fact, an L-galactose dehydrogenase" is inconclusive. Smirnoff's comparison between SEQ. 1 and the putative peptide is based on a subsequence of 18 amino acids out of 319 amino acids in the entire putative peptide sequence (5.6 mol%), wherein the subsequence is found near the N-terminus of the putative protein and thus is less likely to have functional significance relative to a hypothetical subsequence closer to the center of the putative protein sequence.

In summary, Smirnoff does not teach the use of yeast containing an LGDH having at least about 90% similarity or at least about 90% identity to SEQ ID NO:11 or being encoded by a coding region having a structure having at least about 90% identity with SEQ ID NO:12. Therefore, Smirnoff does not teach every element of, and cannot anticipate, the present claims.

8. Final remarks

Applicants submit all pending claims are in condition for allowance. The Examiner is invited to contact the undersigned patent agent at (713) 934-4065 with any questions, comments or suggestions relating to the referenced patent application.

Respectfully submitted,

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